

D. Fitzgerald

#14
3F
6/26/00

1646

RAW SEQUENCE LISTING DATE: 05/31/2000
PATENT APPLICATION: US/09/039,177A TIME: 13:21:57

Input Set : A:\LUD5539.seq.txt
Output Set: N:\CRF3\05312000\I039177A.raw

ENTERED

C--> 3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: MIYAZONO, Kohei
6 IMAMURA, Takeshe
7 TEN DIJKE, Peter
9 (ii) TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE
10 KINASE DOMAINS, CORRESPONDING NUCLEIC
11 ACID MOLECULES, AND THEIR USE
13 (iii) NUMBER OF SEQUENCES: 29
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
17 (B) STREET: 666 Fifth Avenue
18 (C) CITY: New York City
19 (D) STATE: New York
20 (E) COUNTRY: USA
21 (F) ZIP: 10103
C--> 23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
25 (B) COMPUTER: IBM PS/2
26 (C) OPERATING SYSTEM: PC-DOS
27 (D) SOFTWARE: Wordperfect
C--> 29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/039,177A
C--> 31 (B) FILING DATE: 13-Mar-1998
32 (C) CLASSIFICATION: 435
67 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/436,265
36 (B) FILING DATE: October 30, 1995
39 (A) APPLICATION NUMBER: PCT/GB93/02367
40 (B) FILING DATE: November 17, 1993
43 (A) APPLICATION NUMBER: GB 9224057.1
44 (B) FILING DATE: November 17, 1992
47 (A) APPLICATION NUMBER: GB 9304677.9
48 (B) FILING DATE: March 8, 1993
51 (A) APPLICATION NUMBER: GB 9304680.3
52 (B) FILING DATE: March 8, 1993
55 (A) APPLICATION NUMBER: 9311047.6
56 (B) FILING DATE: May 28, 1993
60 (A) APPLICATION NUMBER: 9313763.6
61 (B) FILING DATE: July 2, 1993
64 (A) APPLICATION NUMBER: 9136099.2
65 (B) FILING DATE: August 3, 1993
68 (A) APPLICATION NUMBER: 321344.5
69 (B) FILING DATE: October 15, 1993
71 (viii) ATTORNEY/AGENT INFORMATION:
72 (A) NAME: Mary Anne Schofield
73 (B) REGISTRATION NUMBER: 36,669
74 (C) REFERENCE/DOCKET NUMBER: LUD 5539 - JEL/MAS

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TC 1600 MAIL ROOM

RAW SEQUENCE LISTING

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76 (ix) TELECOMMUNICATION INFORMATION:
 77 (A) TELEPHONE: (212) 318-3000
 78 (B) TELEFAX: (212) 752-5958
 82 (2) INFORMATION FOR SEQ ID NO: 1:
 83 (i) SEQUENCE CHARACTERISTICS:
 84 (A) LENGTH: 1984 base pairs
 85 (B) TYPE: nucleic acid
 86 (C) STRANDEDNESS: unknown
 87 (D) TOPOLOGY: linear
 89 (ii) MOLECULE TYPE: cDNA
 91 (iii) HYPOTHETICAL: NO
 C--> 93 (iv) ANTI-SENSE: NO
 95 (v) FRAGMENT TYPE: internal
 97 (vi) ORIGINAL SOURCE:
 98 (A) ORGANISM: Homo sapiens
 100 (ix) FEATURE:
 101 (A) NAME/KEY: CDS
 102 (B) LOCATION: 283..1791
 104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 106 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
 108 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120
 110 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180
 112 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
 114 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC 294
 115 Met Thr Leu Gly
 116 1
 118 TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG 342
 119 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
 120 5 10 15 20
 122 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT 390
 123 Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
 124 25 30 35
 126 GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA 438
 127 Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
 128 40 45 50
 130 GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC 486
 131 Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
 132 55 60 65
 134 TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC 534
 135 Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
 136 70 75 80
 138 GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC 582
 139 Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
 140 85 90 95 100
 142 CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT 630
 143 Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
 144 105 110 115
 146 GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG 678
 147 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu

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214 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
215 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
216      390      395      400
218 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
219 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
220 405      410      415      420
222 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
223 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
224      425      430      435
226 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
227 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
228      440      445      450
230 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
231 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
232      455      460      465
234 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
235 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
236 470      475      480
238 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
239 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
240 485      490      495      500
242 GTG ATT CAA TAGCCACAGGA GCACCTGATT CCTTCTTGCC TGCAGGGGGC      1831
243 Val Ile Gln
245 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG      1891
247 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCACCC AGCCAAAAAT      1951
249 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA      1984
252 (2) INFORMATION FOR SEQ ID NO: 2:
253   (i) SEQUENCE CHARACTERISTICS:
254       (A) LENGTH: 503 amino acids
255       (B) TYPE: amino acid
256       (D) TOPOLOGY: linear
258   (ii) MOLECULE TYPE: protein
260   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
262 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
263 1      5      10      15
265 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
266      20      25      30
268 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
269      35      40      45
271 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
272      50      55      60
274 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
275 65      70      75      80
277 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
278      85      90      95
280 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
281      100     105     110
283 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
284      115     120     125

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286 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
287      130      135      140
289 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
290 145      150      155      160
292 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
293      165      170      175
295 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
296      180      185      190
298 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
299      195      200      205
301 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
302      210      215      220
304 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
305 225      230      235      240
307 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
308      245      250      255
310 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
311      260      265      270
313 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
314      275      280      285
316 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
317      290      295      300
319 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
320 305      310      315      320
322 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
323      325      330      335
325 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
326      340      345      350
328 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
329      355      360      365
331 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
332      370      375      380
334 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
335 385      390      395      400
337 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
338      405      410      415
340 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
341      420      425      430
343 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
344      435      440      445
346 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
347      450      455      460
349 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
350 465      470      475      480
352 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
353      485      490      495
355 Glu Lys Pro Lys Val Ile Gln
356      500
359 (2) INFORMATION FOR SEQ ID NO: 3:

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VERIFICATION SUMMARY

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Input Set : A:\LUD5539.seq.txt

Output Set: N:\CRF3\05312000\I039177A.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:23 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:93 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:370 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:674 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:993 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1282 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1569 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1844 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2135 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2418 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2693 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2711 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2729 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2747 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2765 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2783 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2801 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26